DNA methylation and methylcytosine oxidation in cell fate decisions.

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Public Summary:
Changes in cellular phenotypes and identities are fundamentally regulated by epigenetic mechanisms including DNA methylation, post-translational histone modifications and chromatin remodeling. Recent genome-wide profiles of the mammalian DNA 'methylome' suggest that hotspots of dynamic DNA methylation changes during cell fate transitions occur at distal regulatory regions with low or intermediate CpG densities. These changes are most prevalent early during the course of cellular differentiation and can be locally influenced by binding of cell-type specific transcription factors. With the advent of next-generation quantitative base-resolution maps of 5-methylcytosine and its oxidized derivatives and better coverage of the genome, we expect to learn more about the true significance of these DNA modifications in the regulation of cell fate choices.

Scientific Abstract:
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